

# Curriculum Vitae

## JUN DING

### CONTACT INFORMATION

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### EDUCATION

<b>Ph.D.</b> in Biostatistics	2010
Department of Biostatistics, University of Michigan, Ann Arbor, MI	
Doctoral advisor: Gonçalo Abecasis	
<b>M.S.</b> in Biostatistics	2005
Department of Biostatistics, University of Michigan, Ann Arbor, MI	
<b>M.S.</b> in Biochemistry	2003
Department of Biochemistry, Case Western Reserve University, Cleveland, OH	
<b>B.S.</b> in Biochemistry	2000
Intensive Training Center, Nanjing University, Nanjing, China	

### PROFESSIONAL EXPERIENCE

**Staff Scientist/Facility Head** Jan 2011 - present  
Human Statistical Genetics Unit, Longitudinal Studies Section, Translational  
Gerontology Branch, National Institute on Aging, NIH  
Human Statistical Genetics Unit, Laboratory of Genetics and Genomics, National  
Institute on Aging, NIH

**Post-doctoral Research Fellow** Oct 2010 - Dec 2010  
Department of Biostatistics, University of Michigan

### PUBLICATIONS

#### Pre-print articles under review/revision

1. Liu X, Longchamps RJ, Wiggins K, Raffield L, Bielak L, Zhao W, Pitsillides AN, Blackwell T, Yao J, Guo X, Kurniansyah N, Thyagarajan B, Pankratz N, Rich SS, Taylor KD, Peyser PA, Heckbert SR, Seshadri S, Cupples LA, Boerwinkle E, Grove

ML, Larson N, Smith JA, Vasan RS, Sofer T, Fitzpatrick AL, Fornage M, **Ding J**, Correa A, Abecasis G, Psaty BM, Wilson JG, Levy D, Rotter JI, Bis JC, Satizabal CL, Arking DE, Liu C (2020). Association of mitochondrial DNA copy number with cardiometabolic diseases in a large cross-sectional study of multiple ancestries. *medRxiv*. doi: <https://doi.org/10.1101/2020.04.20.20016337>

2. Liu C, Fetterman JL, Sun X, Yan K, Liu P, Luo Y, **Ding J**, Zhu J, Levy D (2020). Comparison of mitochondrial DNA sequences derived from whole blood versus lymphoblastoid cell lines. Under revision in *Scientific Reports*.

### Refereed Journal Articles

3. Sun ED, Qian Y, Oppong R, Butler TJ, Zhao J, Chen BH, Tanaka T, Kang J, Sidore C, Cucca F, Bandinelli S, Abecasis GR, Gorospe M, Ferrucci L<sup>#</sup>, Schlessinger D<sup>#</sup>, Goldberg I<sup>#</sup>, **Ding J<sup>#</sup>** (2021). Predicting physiological aging rates from a range of quantitative traits using machine learning. *Aging* 13:23471. PMID: 34718232.  
#corresponding authors
4. Liu C, Fetterman JL, Qian Y, Sun X, Blackwell T, Pitsillides A, Cade BE, Wang H, Raffield LM, Lange LA, Anugu P, Abecasis G, Cupples LA, Redline S, Correa A, Vasan RS, Wilson JG, **Ding J**, Levy D, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium (2021). Presence and transmission of mitochondrial heteroplasmic mutations in human populations of European and African ancestry. *Mitochondrion* 60: 33. PMID: 34303007.
5. Tumasiyan RA, Harish A, Kundu G, Yang J, Ubaida-Mohien C, Gonzalez-Freire M, Kaileh M, Zukley LM, Chia CW, Lyashkov A, Wood WH, Piao Y, Coletta C, **Ding J**, Gorospe M, Sen R, De S, Ferrucci L (2021). Skeletal Muscle Transcriptome in Healthy Aging. *Nature Communications* 12: 2014. PMID: 33795677.
6. Butler TJ, Estep KN, Sommers JA, Maul RW, Moore AZ, Bandinelli S, Cucca F, Tuke MA, Wood AR, Bharti SK, Bogenhagen DF, Yakubovskaya E, Garcia-Diaz M, Guilliam TA, Byrd AK, Raney KD, Doherty AJ, Ferrucci L, Schlessinger D, **Ding J<sup>#</sup>**, Brosh RM<sup>#</sup> (2020). Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis *in vitro*. *Human Molecular Genetics* 29: 1292. PMID: 32191790. #corresponding authors
7. Ntalla I, Weng L, Cartwright JH, Hall AW, ..., (**Ding J** as a co-author), ..., Munroe PB (2020). Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications* 11: 2542. PMID: 32439900.
8. Noordam R, Young WJ, Salman R, Kanters JK, ..., (**Ding J** as a co-author), ..., Warren HR (2019). Effects of Calcium, Magnesium, and Potassium Concentrations on Ventricular Repolarization in Unselected Individuals. *Journal of the American College of Cardiology* 73: 3118. PMID: 31221261.

9. Estep KN, Butler TJ, **Ding J**, Brosh RM (2019). G4-Interacting DNA Helicases and Polymerases: Potential Therapeutic Targets. *Current Medicinal Chemistry* 26: 2881. PMID: 29149833.
10. Orlov NV, Coletta C, van Asten F, Qian Y, **Ding J**, AlGhatri M, Lakatta E, Chew E, Wong W, Swaroop A, Fiorillo E, Delitala A, Marongiu M, Goldberg IG, Schlessinger D (2019). Age-related changes of the retinal microvasculature. *PLoS One* 14: e0215916. PMID: 31048908.
11. Evangelou E, Warren HR, Mosen-Ansorena D, Mifsud B, ..., (**Ding J** as a co-author), ..., Caulfield MJ (2018). Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics* 50: 1412. PMID: 30224653.
12. Moore AZ, **Ding J**, Tuke MA, Wood AR, Bandinelli S, Frayling TM, Ferrucci L (2018). Influence of cell distribution and diabetes status on the association between mitochondrial DNA copy number and aging phenotypes in the InCHIANTI study. *Aging Cell* 17: e12683. PMID: 29047204.
13. Qian Y, Butler TJ, Opsahl-Ong K, Giroux NS, Sidore C, Nagaraja R, Cucca F, Ferrucci L, Abecasis GR, Schlessinger D, **Ding J**<sup>#</sup> (2017). *fastMitoCalc*: an ultra-fast program to estimate mitochondrial DNA copy number from whole-genome sequences. *Bioinformatics* 33: 1399. PMID: 28172616. <sup>#</sup>corresponding author
14. Okbay A, Beauchamp JP, Fontana MA, Lee JJ, ..., (**Ding J** as a co-author), ..., Benjamin DJ (2016). Genome-wide association study identifies 74 loci associated with educational attainment. *Nature* 533: 539. PMID: 27225129.
15. Okbay A, Baselmans BM, De Neve JE, Turley P, ..., (**Ding J** as a co-author), ..., Cesari D (2016). Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics* 48: 624. PMID: 27089181.
16. van den Berg SM, de Moor MH, Verweij KJ, Krueger RF, ..., (**Ding J** as a co-author), ..., Boomsma DI (2016). Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics* 46: 170. PMID: 26362575.
17. **Ding J**<sup>#</sup>, Sidore C, Butler TJ, Wing MK, Qian Y, Meirelles O, Busonero F, Tsoi LC, Maschio A, Angius A, Kang HM, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D<sup>#</sup> (2015). Assessing mitochondrial DNA variation and copy number in lymphocytes of ~2,000 Sardinians using tailored sequencing analysis tools. *PLoS Genetics* 11(7): e1005306. PMID: 26172475. <sup>#</sup>corresponding authors

18. Abdelmohsen K, Panda AC, De S, Grammatikakis I, Kim J, **Ding J**, Noh JH, Kim KM, Mattison JA, de Cabo R, Gorospe M (2015). Circular RNAs in monkey muscle: age-dependent changes. *Aging* 7(11): 903. PMID: 26546448.
19. Genetics of Personality Consortium (including **Ding J**) (2015). Meta-analysis of genome-wide association studies for neuroticism, and the polygenic association with major depressive disorder. *JAMA Psychiatry* 72: 642. PMID: 25993607.
20. Das S, Stuart PE, **Ding J**, Tejasvi T, Li Y, Tsoi LC, Chandran V, Fischer J, Helms C, Duffin KC, Voorhees JJ, Bowcock AM, Krueger GG, Lathrop GM, Nair RP, Rahman P, Abecasis GR, Gladman D, Elder JT (2015). Fine mapping of eight psoriasis susceptibility loci. *European Journal of Human Genetics* 23:844. PMID: 25182136.
21. Huang J, Chen J, Esparza J, **Ding J**, Elder JT, Abecasis GR, Lee Y, Lathrop GM, Moffatt MF, Cookson WOC, Liang L (2015). eQTL mapping identifies insertion- and deletion-specific eQTLs in multiple tissues. *Nature Communications* 6:6821. PMID: 25951796.
22. Tsoi LC, Iyer MK, Stuart PE, Swindell WR, Gudjonsson JE, Tejasvi T, Sarkar MK, Li B, **Ding J**, Voorhees JJ, Kang HM, Nair RP, Chinnaiyan AM, Abecasis GR, Elder JT (2015). Analysis of long non-coding RNAs highlights tissue-specific expression patterns and epigenetic profiles in normal and psoriatic skin. *Genome Biology* 16: 24. PMID: 25723451.
23. Terracciano A, Strait J, Scuteri A, Meirelles O, Sutin AR, Tarasov K, **Ding J**, Marongiu M, Orru M, Pilia MG, Cucca F, Lakatta E, Schlessinger D (2014) Personality traits and circadian blood pressure patterns: a 7-year prospective study. *Psychosomatic Medicine* 76: 237-243. PMID: 24608035.
24. Li B, Tsoi LC, Swindell WR, Gudjonsson JE, Tejasvi T, Johnston A, **Ding J**, Stuart PE, Xing X, Kochkodan JJ, Voorhees JJ, Kang HM, Nair RP, Abecasis GR, Elder JT (2014). Transcriptome Analysis of Psoriasis in a Large Case–Control Sample: RNA-Seq Provides Insights into Disease Mechanisms. *Journal of Investigative Dermatology* 134:1828–1838. PMID: 24441097.
25. Pelosi E, Omari S, Michel M, **Ding J**, Amano T, Forabosco A, Schlessinger D, Ottolenghi C (2013) Constitutively active Foxo3 in oocytes preserves ovarian reserve in mice. *Nature Communications* 4: 1843. PMID: 23673628.
26. Johnston A, Xing X, Swindell WR, Kochkodan J, Riblett M, Nair RP, Stuart PE, **Ding J**, Voorhees JJ, Elder JT and Gudjonsson JE (2013) Susceptibility-associated genetic variation at IL12B enhances Th1 polarization in psoriasis. *Human Molecular Genetics* 22:1807-1815. PMID: 23376980.
27. Meirelles OD, **Ding J**, Tanaka T, Sanna S, Yang HT, Dudekula DB, Cucca F, Ferrucci L, Abecasis G and Schlessinger D (2013) SHAVE: shrinkage estimator

measured for multiple visits increases power in GWAS of quantitative traits.  
*European Journal of Human Genetics* 21:673-679. PMID: 23092954.

28. Tsoi LC, Spain SL, Knight J, Ellinghaus E, Stuart PE, Capon F, **Ding J**, Li Y, Tejasvi T, Gudjonsson JE, Kang HM, Allen MH, McManus R, Novelli G, Samuelsson L, Schalkwijk J, Stähle M, Burden AD, Smith CH, Cork MJ, Estivill X, Bowcock AM, Krueger GG, Weger W, Worthington J, Tazi-Ahnini R, Nestle FO, Hayday A, Hoffmann P, Winkelmann J, Wijmenga C, Langford C, Edkins S, Andrews R, Blackburn H, Strange A, Band G, Pearson RD, Vukcevic D, Spencer CC, Deloukas P, Mrowietz U, Schreiber S, Weidinger S, Koks S, Kingo K, Esko T, Metspalu A, Lim HW, Voorhees JJ, Weichenthal M, Wichmann HE, Chandran V, Rosen CF, Rahman P, Gladman DD, Griffiths CE, Reis A, Kere J; Collaborative Association Study of Psoriasis (CASP); Genetic Analysis of Psoriasis Consortium; Psoriasis Association Genetics Extension; Wellcome Trust Case Control Consortium 2, Nair RP, Franke A, Barker JN, Abecasis GR, Elder JT and Trembath RC (2012) Identification of 15 new psoriasis susceptibility loci highlights the role of innate immunity. *Nature Genetics* 44:1341-1348.
29. Voight BF, Kang HM, **Ding J**, Palmer CD, Sidore C, Chines PS, Burtt NP, Fuchsberger C, Li Y, Erdmann J, Frayling TM, Heid IM, Jackson AU, Johnson T, Kilpelainen TO, Lindgren CM, Morris AP, Prokopenko I, Randall JC, Saxena R, Soranzo N, Speliotes EK, Teslovich TM, Wheeler E, Maguire J, Parkin M, Potter S, Rayner NW, Robertson N, Stirrups K, Winckler W, Sanna S, Mulas A, Nagaraja R, Cucca F, Barroso I, Deloukas P, Loos RJ, Kathiresan S, Munroe PB, Newton-Cheh C, Pfeifer A, Samani NJ, Schunkert H, Hirschhorn JN, Altshuler D, McCarthy MI, Abecasis GR and Boehnke M (2012) The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. *PLoS Genetics* 8: e1002793.
30. Clarke L, Zheng-Bradley X, Smith R, Kulesha E, Xiao C, Toneva I, Vaughan B, Preuss D, Leinonen R, Shumway M, Sherry S, Flücke P; 1000 Genomes Project Consortium (including **Ding J**) (2012) The 1000 Genomes Project: data management and community access. *Nature Methods* 9: 459-462.
31. Zhang M, Liang L, Morar N, Dixon AL, Lathrop GM, **Ding J**, Moffatt MF, Cookson WO, Kraft P, Qureshi AA and Han J (2011) Integrating pathway analysis and genetics of gene expression for genome-wide association study of basal cell carcinoma. *Human Genetics* 131: 615-623.
32. **Ding J<sup>#</sup>**, Gudjonsson JE, Liang L, Stuart PE, Li Y, Chen W, Weichenthal M, Ellinghaus E, Franke A, Cookson W, Nair RP, Elder JT and Abecasis GR<sup>#</sup> (2010) Gene expression in skin and lymphoblastoid cells: refined statistical method reveals extensive overlap in cis-eQTL signals. *American Journal of Human Genetics* 87: 779-789. <sup>#</sup> corresponding authors

33. Zawistowski M, Gopalakrishnan S, **Ding J**, Li Y, Grimm S and Zollner S (2010) Extending rare-variant testing strategies: analysis of noncoding sequence and imputed genotypes. *American Journal of Human Genetics* 87: 604-617.
34. 1000 Genomes Project Consortium (including **Ding J**) (2010) A map of human genome variation from population-scale sequencing. *Nature* 467:1061-1073.
35. Stuart PE, Nair RP, Ellinghaus E, **Ding J**, Tejasvi T, Gudjonsson JE, Li Y, Weidinger S, Eberlein B, Gieger C, Wichmann HE, Kunz M, Ike R, Krueger GG, Bowcock AM, Mrowietz U, Lim HW, Voorhees JJ, Abecasis GR, Weichenthal M, Franke A, Rahman P, Gladman D and Elder JT (2010) Genome-wide association analysis identifies three psoriasis susceptibility loci. *Nature Genetics* 42: 1000-1004.
36. Ellinghaus E, Ellinghaus D, Stuart PE, Nair RP, Debrus S, Raelson JV, Belouchi M, Fournier H, Reinhard C, **Ding J**, Li Y, Weidinger S, Eberlein B, Kunz M, Rahman P, Gladman D, Gieger C, Wichmann HE, Karlsen TH, Kabelitz D, Abecasis GR, Elder JT, Schreiber S, Weichenthal M and Franke A (2010) Genome-wide association study identifies a psoriasis susceptibility locus at TRAF3IP2. *Nature Genetics* 42: 991-995.
37. Li Y, Willer CJ, **Ding J**, Scheet P and Abecasis GR (2010) MaCH: using sequence and genotype data to estimate haplotypes and unobserved genotypes. *Genetic Epidemiology* 34: 816-834.
38. Gudjonsson JE, Johnston A, Stoll SW, Riblett MB, Xing X, Kochkodan JJ, **Ding J**, Nair RP, Aphale A, Voorhees JJ and Elder JT (2010) Evidence for altered Wnt signaling in psoriatic skin. *Journal of Investigative Dermatology* 130: 1849-1859.
39. Gudjonsson JE\*, **Ding J\***, Johnston A, Tejasvi T, Guzman AM, Nair RP, Voorhees JJ, Abecasis GR and Elder JT (2010) Assessment of the psoriatic transcriptome in a large sample: additional regulated genes and comparisons with in vitro models. *Journal of Investigative Dermatology* 130: 1829-1840. \*joint first author
40. Nair RP\*, Duffin KC\*, Helms C\*, **Ding J\***, Stuart PE, Goldgar D, Gudjonsson JE, Li Y, Tejasvi T, Feng B, Ruether A, Schreiber S, Weichenthal M, Gladman D, Rahman P, Schrödi SJ, Prahalad S, Guthery SL, Fischer J, Liao W, Kwok P, Menter A, Lathrop GM, Wise C, Begovich AB, Voorhees JJ, Elder JT, Krueger GG, Bowcock AM, Abecasis GR for the Collaborative Association Study of Psoriasis (2009) Genome-wide scan reveals association of psoriasis with IL-23 and NF-κB pathways. *Nature Genetics* 41:199-204. \*joint first author
41. Gudjonsson JE\*, **Ding J\***, Li X, Nair RP, Tejasvi T, Qin ZS, Ghosh D, Aphale A, Gumucio DL, Voorhees JJ, Abecasis GR and Elder JT (2009) Global gene expression analysis reveals evidence for decreased lipid biosynthesis and increased innate immunity in uninvolved psoriatic Skin. *Journal of Investigative Dermatology* 129:2795-2804. \*joint first author

42. Nair RP, **Ding J**, Duffin KC, Helms C, Voorhees JJ, Krueger GG, Bowcock AM, Abecasis GR and Elder JT (2009). Psoriasis bench to bedside: genetics meets immunology. *Archives of Dermatology* 145:462-464.
43. Gudjonsson JE, Aphale A, Grachtchouk M, **Ding J**, Nair RP, Wang T, Voorhees JJ, Dlugosz AA and Elder JT (2009) Lack of evidence for activation of the Hedgehog pathway in psoriasis. *Journal of Investigative Dermatology* 129: 635-640.
44. Meyer-Lindenberg A, Nichols T, Callicott JH, **Ding J**, Kolachana B, Buckholtz J, Mattay VS, Egan M and Weinberger DR (2006) Impact of complex genetic variation in COMT on human brain function. *Molecular psychiatry* 11: 867–877.
45. Jiang P, Chen L, Lin J, Liu Q, **Ding J**, Gao X and Guo Z (2002) Novel zinc fluorescent probe bearing dansyl and aminoquinoline groups. *Chemical Communications* 7: 1424-1425.

## INVITED TALKS

1. Assessing mitochondrial DNA variation using tailored sequencing analysis tools. *Department of Biostatistics, Bioinformatics, and Biomathematics, Georgetown University, Washington D.C.* December 2017
2. Bioinformatic assessment of mitochondrial DNA variation and copy number from whole-genome sequence data. *Department of Systems Medicine, Keio University, Tokyo, Japan.* May 2017
3. Assessing mitochondrial DNA variation and copy number in 2,000 Sardinians using tailored sequencing analysis tools. *Biostatistics and Bioinformatics Branch, Division of Intramural Population Health Research, Eunice Kennedy Shriver National Institute of Child Health and Human Development (NICHD), NIH.* June 2016
4. Assessing mitochondrial DNA variation and copy number by tailored sequencing analysis tools. *Center for Inherited Disease Research, Johns Hopkins University, Baltimore, MD.* November 2014
5. A DNA variant caller adapted to assess mitochondrial DNA variation using whole-genome sequencing data. *2013 ICSA Joint Statistics Conference, Bethesda, MD.* June 2013
6. A DNA variant caller adapted to assess mitochondrial DNA variation using whole-genome sequencing data. *Biophysics Seminar Series, George Washington University, Washington, DC.* April 2013
7. An integrated genetic study of psoriasis: genome-wide association and expression-QTL analyses. *Department of Preventive Medicine, University of Southern California, Los Angeles, CA.* February 2010

8. An integrated genetic study of psoriasis: genome-wide association and expression-QTL analyses. *National Institute on Aging, Baltimore, MD*. January 2010

## PRESENTATIONS

1. **Ding J**, Sun ED, Zhao J, Abecasis GR, Cucca F, Goldberg IG, Schlessinger D, Measuring the rate and heritability of aging using machine learning methods Presented at the annual meeting of The American Society of Human Genetics, October 2017 (poster).
2. **Ding J**, Qian Y, Sidore C, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D, *mini-mitoCalc*: an ultra-fast program to estimate mitochondrial DNA copy number from whole-genome sequences. Presented at the annual meeting of The American Society of Human Genetics, October 2016 (poster).
3. Zhang P, Ling H, Hetrick K, Pugh E, Witmer D, **Ding J**, Sobreira N, Valle D, Doheny K, Calling mitochondrial DNA (mtDNA) variants from whole exome sequencing data. Presented at the annual meeting of The American Society of Human Genetics, October 2015 (poster).
4. **Ding J**, Sidore C, Butler TJ, Wing MK, Meirelles O, Qian Y, Busonero F, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D, Assessing mitochondrial DNA variation and copy number in lymphocytes of 2,077 Sardinians using tailored sequencing analysis tools. Presented at the annual meeting of The American Society of Human Genetics, October 2014 (poster).
5. **Ding J**, Sidore C, Meirelles O, Wing MK, Busonero F, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D, A DNA variant caller adapted to assess mitochondrial DNA variation in lymphocytes from 2,000 Sardinians. Presented at The Biology of Genomes meeting, Cold Spring Harbor Laboratory, May 2014 (poster).
6. **Ding J**, Sidore C, Meirelles O, Wing MK, Busonero F, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D, A DNA variant caller adapted to assess mitochondrial DNA variation from whole-genome sequencing data. Presented at the 2014 ENAR Spring Meeting, March 2014 (talk).
7. **Ding J**, Sidore C, Meirelles O, Trost MK, Busonero F, Nagaraja R, Cucca F, Abecasis GR, Schlessinger D, A DNA variant caller adapted to assess mitochondrial DNA variation in lymphocytes from 1,000 Sardinians. Presented at the annual meeting of The American Society of Human Genetics, November 2012 (platform).
8. Meirelles O, **Ding J**, Tanaka T, Sanna S, Yang H, Dudekula DB, Cucca F, Ferrucci L, Abecasis GR, Schlessinger D, SHAVE - Shrinkage Estimator Measured for Multiple Visits Increases Power in GWAS of Quantitative Traits. Presented at the annual meeting of The American Society of Human Genetics, November 2012 (poster).

9. Tsoi LC, Spain SL, Knight J, Ellinghaus E, Stuart PE, Capon F, **Ding J**, Li Y, Tejasvi T, Gudjonsson JE, Kang HM, Bowcock AM, Mrowietz U, Koks S, Esko T, Voorhees JJ, Weichenthal M, Rahman P, Gladman D, Griffiths CEM, Reis A, Kere1 J, Nair RP, Franke A, Barker JNWN, Abecasis GR, Elder JT, Trembath RC, Genetic Analysis of Psoriasis Consortium, Wellcome Trust Case Control Consortium 2, Fifteen novel psoriasis susceptibility loci: disease-specific signals highlight the role of innate immunity. Presented at the annual meeting of The American Society of Human Genetics, November 2012 (platform).
10. Das S, Stuart PE, **Ding J**, Tejasvi T, Li Y, Tsoi LC, Chandran V, Fischer J, Helms C, Duffin KC, Voorhees JJ, Bowcock AM, Krueger GG, Lathrop GM, Nair RP, Rahman P, Abecasis GR, Gladman D, Elder JT, Fine-mapping of eight psoriasis susceptibility loci. Presented at the annual meeting of The American Society of Human Genetics, November 2012 (poster).
11. Chen H, Esparza J, **Ding J**, Abecasis G, Lee Y, Moffatt MF, Cookson WOC, Liang L, Meta-analysis on eQTL mapping identify common and tissue specific eQTLs in LCL, PBMC and skin tissues. Presented at the annual meeting of The American Society of Human Genetics, October 2011 (platform).
12. Tsoi L, Nair R, Li B, **Ding J**, Gudjonsson J, Stuart P, Tejasvi T, Kang H, Abecasis G, Elder JT, Large-scale transcriptome analysis using RNA-seq reveals new insights into psoriasis biology. Presented at the annual meeting of The American Society of Human Genetics, October 2011 (platform).
13. Nair RP, Stuart PE, Tejasvi T, Shaiq PA, Qamar R, Raja GK, Kullavanijaya P, **Ding J**, Li Y, Voorhees JJ, Abecasis GR, Elder JT, A Single SNP Surrogate for HLA-Cw6 Genotyping in Diverse Populations. Presented at the annual meeting of The American Society of Human Genetics, October 2011 (poster).
14. **Ding J**, Abecasis GR, A novel method for estimating the overlap of eQTLs between two tissues, with application to skin and lymphoblastoid cells. Presented at the annual meeting of The American Society of Human Genetics, November 2010 (poster).
15. **Ding J**, Abecasis GR, A method for estimating the overlap of eQTLs between two tissues, with application to skin and lymphoblastoid cells. Presented at the Joint Statistical Meetings of The American Statistical Association, July 2010 (oral presentation).
16. **Ding J**, Gudjonsson JE, Liang L, Stuart PE, Chen W, Nair RP, Elder JT, Abecasis GR, A method to estimate the sharing of eQTLs between tissues, with application to skin and lymphoblastoid cells. Presented at the annual meeting of The American Society of Human Genetics, October 2009 (poster).

17. **Ding J**, Gudjonsson JE, Liang L, Nair RP, Chen W, Stuart PE, Voorhees JJ, Elder JT, Abecasis GR, Genome-wide association study of gene expression in human skin. Presented at The Biology of Genomes meeting, Cold Spring Harbor Laboratory, May 2009 (poster).
18. **Ding J**, Gudjonsson JE, Liang L, Nair RP, Stuart PE, Voorhees JJ, Elder JT, Abecasis GR, A genome-wide association study of gene expression in skin. Presented at the annual meeting of The American Society of Human Genetics, November 2008 (poster).
19. Bowcock AM, **Ding J**, Duffin KC, Nair RP, Stuart PE, Goldgar D, Helms C, Tejasvi T, Gudjonsson JE, Menter A, Voorhees JJ, Krueger GG, Elder JT, Abecasis GR for the Collaborative Association Study of Psoriasis, Genome-wide association scan of psoriasis implicates genes associated with T cell differentiation. Presented at the annual meeting of The American Society of Human Genetics, November 2008 (platform).
20. **Ding J** and Abecasis GR, Searching for master regulatory variants of gene expression. Presented at the annual meeting of The American Society of Human Genetics, October 2007 (platform).
21. Li Y, Willer CJ, **Ding J**, Scheet P and Abecasis GR, In silico genotyping for genome-wide association studies. Presented at the annual meeting of The American Society of Human Genetics, October 2007 (poster).
22. **Ding J**, Gudjonsson JE, Nair R, Stuart P, Ghosh D, Voorhees JJ, Abecasis GR and Elder JT, High-throughput gene expression analysis of skin from psoriatic patients and normal controls. Presented at the annual meeting of The American Society of Human Genetics, October 2006 (poster).
23. Li Y, **Ding J** and Abecasis GR, Mach 1.0: rapid haplotype reconstruction and missing genotype inference. Presented at the annual meeting of The American Society of Human Genetics, October 2006 (poster).

## SERVICE AND PROFESSIONAL ACTIVITIES

### **Student Mentoring:**

Vidur Kailash (NIA postbaccalaureate student)	Sept 2020 – Aug 2021
Larry Reser (NIA postbaccalaureate student)	Sept 2018 – Aug 2020
Nicholas S. Giroux (NIA summer student and student fellow)	Jun 2016 – Aug 2018
Jesse Y. Zhao (NIA postbaccalaureate student)	Aug 2016 – Aug 2017
Krista Opsahl-Ong (NIA summer student, winner of the Barbara A. Hughes Award for Scientific Excellence in the NIA Summer program)	Jun 2015 - Aug 2015
Yuho Doh (NIA postbaccalaureate student)	Aug 2014 - Feb 2015
Thomas J. Butler (NIA summer student and postbaccalaureate student)	

Jun 2013 - Aug 2014

**Editorial Board Member:**

*Scientific Reports*

*Frontiers in Aging*

**Guest Associate Editor:**

*Circulation*

**Ad hoc Reviewer:**

*Aging*

*Annals of Human Genetics*

*Bioinformatics*

*Biostatistics*

*Genome Research*

*Human Genetics*

*Human Mutation*

*International Journal of Biological Sciences*

*Journal of Gerontology: Medical Sciences*

*Journal of Investigative Dermatology*

*Molecular Psychiatry*

*PLoS Genetics*

*PLoS One*

*Science*

**Community Service at NIA**

Member, Biomedical Data Science Network

2017 - present

Organizer, Quantitative Science Seminar Series

2015 - present

Committee Member, Postbaccalaureate Advisory Committee

2012 - present

**Graduate Student Coordinator**

2006 - 2010

Interdisciplinary Group Seminar, University of Michigan

**Curriculum Committee Member**

2005 - 2006

**Computing Committee Member**

2004 - 2005

**Student Activities Committee Member**

2003 - 2004

Department of Biostatistics, University of Michigan

**Chairperson**

2000

Seminar of Life Sciences, Nanjing University

**AWARDS AND HONORS**

**Rackham Travel Grant**

2006, 2008, 2009, 2010

Rackham Graduate School, University of Michigan

<b>Outstanding First-Year Masters Student</b>	2004
<b>Eli Lilly Scholarship</b>	2003
Department of Biostatistics, University of Michigan	
<b>Most Creative Student Award of Nanjing University</b>	1998, 1999
Nanjing University	
<b>Special Award for Best Student</b>	1997
<b>First-Class People's Scholarship</b>	1997
Intensive Training Center, Nanjing University	

## **PROFESSIONAL ORGANIZATIONS**

American Society of Human Genetics  
 American Statistical Association

## **COMPUTING SKILLS**

C/C++, Matlab, Perl, R/S-PLUS, SAS, Unix/Linux, Windows